

(FILE 'HOME' ENTERED AT 11:44:35 ON 20 SEP 2006)

FILE 'AGRICOLA, CABA, CAPLUS, BIOSIS' ENTERED AT 11:44:52 ON 20 SEP 2006

L1 15 S ((HATZFELD Y?)OR (HATZFELD,Y?))/AU AND PROMOTER  
L2 6 S L1 AND RICE  
L3 4 DUP REM L2 (2 DUPLICATES REMOVED)  
L4 32 S ((BROEKAERT W?)OR (BROEKAERT, W?))/AU AND PROMOTER  
L5 7 S L4 AND RICE  
L6 5 DUP REM L5 (2 DUPLICATES REMOVED)  
L7 3447 S HIGH MOBILITY GROUP PROTEIN  
L8 259 S L7 AND PLANT  
L9 164 S L7 AND (RICE OR MAIZE OR WHEAT OR ARABIDOPSIS OR TOBACCO OR  
L10 94 DUP REM L9 (70 DUPLICATES REMOVED)  
L11 22 S L10 AND PROMOTER

## EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L4	364	high mobility group protein	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	ADJ	ON	2006/09/20 11:40
L5	2	L4 and L2	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	ADJ	ON	2006/09/20 11:40
L6	159	L4 and plant	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	ADJ	ON	2006/09/20 11:40
L7	148	L6 and (expression pattern or promoter)	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	ADJ	ON	2006/09/20 11:41
L8	44	L6 and (expression pattern or promoter)and promoter.CLM.	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	ADJ	ON	2006/09/20 11:42
L9	38	L6 and rice	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	ADJ	ON	2006/09/20 11:42
L10	4512	promoter.CLM. and (rice or oryza sativa)	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	ADJ	ON	2006/09/20 11:56
L11	4474	L1 and promoter	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	ADJ	ON	2006/09/20 11:56
L12	0	L11 and high mobility protein	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	ADJ	ON	2006/09/20 11:57

## EAST Search History

L13	18	L11 and high mobility group protein	US-PGPUB; USPAT; USOCR; EPO; JPO; DERWENT	ADJ	ON	2006/09/20 11:57
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OM nucleic - nucleic search, using sw model

Run on: August 31, 2006, 00:43:06 ; Search time 6763 Seconds  
(without alignments)  
10684.694 Million cell updates/sec

Title: US-10-525-647-18

Perfect score: 1130

Sequence: 1 catgcggctaatgttagatgc.....ccttctcgcaggattcagcc 1130

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size : 30

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:  
1: gb\_env:  
2: gb\_pat:  
3: gb\_ph:  
4: gb\_pl:  
5: gb\_pr:  
6: gb\_ro:  
7: gb\_sts:  
8: gb\_sy:  
9: gb\_un:  
10: gb\_vi:  
11: gb\_ov:  
12: gb\_htg:  
13: gb\_in:  
14: gb\_om:  
15: gb\_ba:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result		Query					Description
No.	Score	Match	Length	DB	ID		
	1	1130	100.0	1130	2	CQ857665	CQ857665 Sequence
c	2	1130	100.0	101546	12	AP004004	AP004004 Oryza sat
	3	1130	100.0	110000	4	AP008212_304	Continuation (305)
	4	1130	100.0	166700	4	AP004685	AP004685 Oryza sat
	5	294	26.0	3659	4	AY262827	AY262827 Oryza sat
	6	231	20.4	998	4	AK068898	AK068898 Oryza sat
	7	139	12.3	913	4	AK062226	AK062226 Oryza sat
	8	119	10.5	964	2	CQ857687	CQ857687 Sequence
	9	115	10.2	871	2	E14787	E14787 cDNA encodi
	10	66	5.8	869	4	AF093632	AF093632 Oryza sat
	11	55	4.9	918	4	AF541859	AF541859 Oryza sat
	12	32	2.8	101080	12	BX004860	BX004860 Danio rer
	13	32	2.8	101241	11	AL845510	AL845510 Zebrafish
	14	32	2.8	142509	12	AC117942	AC117942 Tetraodon
	15	32	2.8	173964	12	AC161299	AC161299 Atelerix
c	16	32	2.8	177519	6	AC132113	AC132113 Mus muscu
	17	32	2.8	181197	11	BX005330	BX005330 Zebrafish
	18	32	2.8	191638	6	AL663062	AL663062 Mouse DNA
	19	32	2.8	200967	12	AP003638	AP003638 Mus muscu
c	20	32	2.8	207115	12	AC121004	AC121004 Rattus no
	21	32	2.8	209838	6	AC101882	AC101882 Mus muscu
	22	32	2.8	214102	12	AC135021	AC135021 Rattus no
c	23	32	2.8	219072	6	AC155286	AC155286 Mus muscu
c	24	32	2.8	227625	12	AC094806	AC094806 Rattus no
c	25	32	2.8	230573	6	AC122883	AC122883 Mus muscu
	26	32	2.8	239078	12	AC098203	AC098203 Rattus no
c	27	32	2.8	246375	12	AC097808	AC097808 Rattus no
c	28	32	2.8	246880	12	AC110111	AC110111 Rattus no
c	29	32	2.8	249021	12	AC094500	AC094500 Rattus no
	30	32	2.8	250384	12	AC102955	AC102955 Rattus no
c	31	32	2.8	261990	12	AC111513	AC111513 Rattus no
	32	31	2.7	66657	12	AC118049	AC118049 Mus muscu
c	33	31	2.7	129369	6	AL732472	AL732472 Mouse DNA
c	34	31	2.7	140552	6	AC164166	AC164166 Mus muscu
	35	31	2.7	158294	6	AC132293	AC132293 Mus muscu
c	36	31	2.7	181320	6	CT030736	CT030736 Mouse DNA
c	37	31	2.7	183031	6	AC126795	AC126795 Mus muscu
	38	31	2.7	188960	6	AC144921	AC144921 Mus muscu
c	39	30	2.7	136911	6	AC156399	AC156399 Mus muscu
c	40	30	2.7	139781	12	AC122437	AC122437 Mus muscu
	41	30	2.7	163916	6	AC141887	AC141887 Mus muscu
c	42	30	2.7	166333	6	AL513470	AL513470 Mouse DNA
c	43	30	2.7	181625	6	AC162692	AC162692 Mus muscu
c	44	30	2.7	217841	12	AC095995	AC095995 Rattus no
	45	30	2.7	218443	12	AC136028	AC136028 Rattus no

## ALIGNMENTS

RESULT 1  
CQ857665

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OM nucleic - nucleic search, using sw model

Run on: August 31, 2006, 00:39:47 ; Search time 814 Seconds  
(without alignments)  
9678.920 Million cell updates/sec

Title: US-10-525-647-18

Perfect score: 1130

Sequence: 1 catgcggctaatgttagatgc.....ccttctcgccaggattcagcc 1130

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 5244920 seqs, 3486124231 residues

Word size : 30

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_8:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*
- 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1130	100.0	1130	13	ADR73675	Adr73675 Rice prom
2	1130	100.0	1606	14	AEC16154	Aec16154 Rice HMG1
3	231	20.4	998	14	AEC16155	Aec16155 Rice HMG1
4	119	10.5	964	13	ADR73697	Adr73697 Rice prom
5	115	10.2	871	2	AAV12741	Aav12741 RBE1 tran
6	58	5.1	812	10	ADK58252	Adk58252 Plant DNA
7	55	4.9	595	10	ADK54154	Adk54154 Plant DNA
8	55	4.9	622	10	ADK54152	Adk54152 Plant DNA
9	55	4.9	797	10	ADK58241	Adk58241 Plant DNA

## ALIGNMENTS

## RESULT 1

ADR73675

ID ADR73675 standard; DNA; 1130 BP.

XX

AC ADR73675;

XX

DT 04-NOV-2004 (first entry)

XX

DE Rice promoter high mobility protein.

XX

KW promoter; rice promoter; genetic construct; expression cassette;  
KW transgenic plant; ds.

XX

OS Oryza sativa.

XX

PN WO2004070039-A2.

XX

PD 19-AUG-2004.

XX

PF 04-FEB-2004; 2004WO-EP050081.

XX

PR 04-FEB-2003; 2003EP-00075331.

XX

PA (CROP-) CROPDFSIGN NV.

XX

PI Hatzfeld Y, Broekaert W;

XX

DR WPI; 2004-604455/58.

XX

PT New rice promoters, useful for driving and/or regulating expression of  
PT nucleic acids and for producing transgenic plants.

XX

PS Claim 1; SEQ ID NO 18; 48pp; English.

XX

CC The present invention relates to an isolated promoter capable of driving  
CC and/or regulating expression. The isolated promoter are rice promoter  
CC comprising any of the sequences of SEQ ID NOS: 1-22. Sequences are not  
CC defined in the specification. The isolated nucleic acids or promoter is

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OM nucleic - nucleic search, using sw model

Run on: August 31, 2006, 00:51:16 ; Search time 340 Seconds  
(without alignments)  
6218.685 Million cell updates/sec

Title: US-10-525-647-18

Perfect score: 1130

Sequence: 1 catgcggctaatgttagatgc.....ccttctcgccaggattcagcc 1130

### Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size : 30

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

2: /EMC Celerra SID

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3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	% Query	Description
-----							
No matches found							

Search completed: August 31, 2006, 01:31:41  
Job time : 340 secs

SCORE 1.3 BuildDate: 12/06/2005

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OM nucleic - nucleic search, using sw model

Run on: August 31, 2006, 01:11:49 ; Search time 1470 Seconds  
(without alignments)  
9445.597 Million cell updates/sec

Title: US-10-525-647-18

Perfect score: 1130

Sequence: 1 catgcggctaatgttagatgc.....ccttctcgcaggattcagcc 1130

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 18892170 seqs, 6143817638 residues

Word size : 30

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_NA\_Main:  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*

9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*

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11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*

12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*

13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*

14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*

15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*

16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	% Query						Description
	No.	Score	Match	Length	DB	ID	
<hr/>							
1	94	8.3	272	8	US-10-437-963-241		Sequence 241, App
2	58	5.1	812	10	US-10-487-901-5635		Sequence 5635, Ap
3	55	4.9	595	10	US-10-487-901-1537		Sequence 1537, Ap
4	55	4.9	622	10	US-10-487-901-1535		Sequence 1535, Ap
5	55	4.9	797	10	US-10-487-901-5624		Sequence 5624, Ap
6	35	3.1	345	8	US-10-437-963-29124		Sequence 29124, A

## ALIGNMENTS

## RESULT 1

US-10-437-963-241  
; Sequence 241, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 241  
; LENGTH: 272  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(272)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_10021C.1  
US-10-437-963-241

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OM nucleic - nucleic search, using sw model

Run on: August 31, 2006, 01:26:06 ; Search time 315 Seconds  
(without alignments)  
5915.462 Million cell updates/sec

Title: US-10-525-647-18

Perfect score: 1130

Sequence: 1 catgcggctaattgttagatgc.....ccttctcgcaggattcagcc 1130

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2281053 seqs, 824500224 residues

Word size : 30

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_NA\_New:\*

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1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	1130	100.0	1130	6	US-10-525-647-18	Sequence 18, Appl
2	231	20.4	998	6	US-10-449-902-18506	Sequence 18506, A
3	139	12.3	913	6	US-10-449-902-5027	Sequence 5027, Ap
4	119	10.5	964	6	US-10-525-647-40	Sequence 40, Appl

## ALIGNMENTS

## RESULT 1

US-10-525-647-18

; Sequence 18, Application US/10525647  
; Publication No. US20060112442A1  
; GENERAL INFORMATION:  
; APPLICANT: CropDesign N.V.  
; TITLE OF INVENTION: Rice promoters  
; FILE REFERENCE: CD-071-PCT  
; CURRENT APPLICATION NUMBER: US/10/525,647  
; CURRENT FILING DATE: 2005-02-24  
; PRIOR APPLICATION NUMBER: EP 03075331.3  
; PRIOR FILING DATE: 2003-02-04  
; NUMBER OF SEQ ID NOS: 88  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 1130  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: PRO0170 - High mobility group protein

US-10-525-647-18

Query Match 100.0%; Score 1130; DB 6; Length 1130;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CATGGGCTAATGTAGATGCTCACTGGCTAGTAGTAAGGTACTCCAGTACATTATGGAA	60
Db	1	CATGGGCTAATGTAGATGCTCACTGGCTAGTAGTAAGGTACTCCAGTACATTATGGAA	60
Qy	61	TATACAAAGCTGTAATACTCGTATCAGCAAGAGAGAGGGCACACAAGTTGAGCAGTAGCA	120
Db	61	TATACAAAGCTGTAATACTCGTATCAGCAAGAGAGAGGGCACACAAGTTGAGCAGTAGCA	120
Qy	121	CAGGATTAGAAAACGGGACGACAATAGTAATGGAAAAACAAAAAAACAAGGAAACA	180
Db	121	CAGGATTAGAAAACGGGACGACAATAGTAATGGAAAAACAAAAAAACAAGGAAACA	180
Qy	181	CATGGCAATATAATGGAGAAATCACAAGAGGAACAGAACATCCGGCAATACGCTGCGAAA	240
Db	181	CATGGCAATATAATGGAGAAATCACAAGAGGAACAGAACATCCGGCAATACGCTGCGAAA	240
Qy	241	GTACTCGTACGTAAAAAGAGGCGCATTGATGTGGACAGCGTGCAGCAGAACAGCAGG	300
Db	241	GTACTCGTACGTAAAAAGAGGCGCATTGATGTGGACAGCGTGCAGCAGAACAGCAGG	300
Qy	301	GATTTGAAACCACCAAATCCACCACTGCAAACCTTCAAACGAGGCCATGGTTGAAGCA	360

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OM nucleic - nucleic search, using sw model

Run on: August 31, 2006, 00:47:10 ; Search time 5237 Seconds  
(without alignments)  
12065.848 Million cell updates/sec

Title: US-10-525-647-18  
Perfect score: 1130  
Sequence: 1 catgcggctaatgttagatgc.....ccttctcgcaggattcagcc 1130

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 48236798 seqs, 27959665780 residues

Word size : 30

Total number of hits satisfying chosen parameters: 485

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:  
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 2: gb\_est3:  
 3: gb\_est4:  
 4: gb\_est5:  
 5: gb\_est6:  
 6: gb\_htc:  
 7: gb\_est2:  
 8: gb\_est7:  
 9: gb\_est8:  
 10: gb\_est9:  
 11: gb\_gss1:  
 12: gb\_gss2:  
 13: gb\_gss3:  
 14: gb\_gss4:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	165	14.6	574	5	CF279360	CF279360 14ETL--05
2	165	14.6	615	5	CF314657	CF314657 HD--03-E0
3	158	14.0	440	5	CF292390	CF292390 30DGS--01
4	158	14.0	859	4	CB675811	CB675811 OSJNEe11M
5	145	12.8	533	5	CF281141	CF281141 14ETL--08
6	145	12.8	603	5	CF282431	CF282431 14ETL--09
7	144	12.7	432	5	CF277714	CF277714 14ETL--03
8	144	12.7	569	5	CF282280	CF282280 14ETL--09
9	144	12.7	651	5	CF291071	CF291071 14ROOT--0
10	144	12.7	660	5	CF292534	CF292534 30DGS--01
11	140	12.4	575	5	CF312650	CF312650 ABF--08-H
12	140	12.4	576	5	CF296977	CF296977 30DGS--07
13	140	12.4	586	5	CF295516	CF295516 30DGS--05
14	140	12.4	608	5	CF308019	CF308019 ABF--01-K
15	140	12.4	612	5	CF312423	CF312423 ABF--08-C
16	140	12.4	646	5	CF312873	CF312873 ABF--08-M
17	140	12.4	655	4	CB685301	CB685301 OSJNEf15J
18	139	12.3	492	5	CF277720	CF277720 14ETL--03
19	139	12.3	555	5	CF312341	CF312341 ABF--07-P
20	139	12.3	575	5	CF311877	CF311877 ABF--07-F
21	139	12.3	576	5	CF291117	CF291117 14ROOT--0
22	139	12.3	591	5	CF281129	CF281129 14ETL--08
23	139	12.3	622	5	CF277475	CF277475 14ETL--03
24	139	12.3	652	5	CF293518	CF293518 30DGS--02
25	137	12.1	621	5	CF279594	CF279594 14ETL--05
26	137	12.1	657	5	CF292592	CF292592 30DGS--01
27	137	12.1	670	5	CF277460	CF277460 14ETL--03
28	136	12.0	295	5	CI298665	CI298665 CI298665
29	136	12.0	309	5	CF296107	CF296107 30DGS--06
30	136	12.0	311	8	CV732879	CV732879 FLO--07-I
31	136	12.0	348	5	CI300124	CI300124 CI300124
32	136	12.0	355	8	CV729959	CV729959 FLO--03-E
33	136	12.0	358	5	CF308797	CF308797 ABF--02-M
34	136	12.0	394	5	CI288540	CI288540 CI288540
35	136	12.0	402	5	CF295060	CF295060 30DGS--04
36	136	12.0	423	5	CF296753	CF296753 30DGS--07
37	136	12.0	424	5	CF336184	CF336184 JMT--06-C
38	136	12.0	489	5	CF296650	CF296650 30DGS--07
39	136	12.0	489	5	CF309847	CF309847 ABF--04-D
40	136	12.0	494	5	CF278922	CF278922 14ETL--05
41	136	12.0	494	5	CF297458	CF297458 30DGS--08
42	136	12.0	494	5	CF297531	CF297531 30DGS--08
43	136	12.0	495	5	CF312624	CF312624 ABF--08-H
44	136	12.0	517	5	CF294173	CF294173 30DGS--03
45	136	12.0	528	5	CF295396	CF295396 30DGS--05

## ALIGNMENTS

RESULT 1

CF279360

LOCUS

CF279360

574 bp

mRNA

linear

EST 14-AUG-2003

# SCORE Search Results Details for Application 10525647 and Search Result us-10-525-647- 18.rng.

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OM nucleic - nucleic search, using sw model

Run on: August 31, 2006, 00:10:55 ; Search time 842 Seconds  
(without alignments)  
9357.056 Million cell updates/sec

Title: US-10-525-647-18

Perfect score: 1130

Sequence: 1 catgcggctaatgttagatgc.....ccttctcgcaggattcagcc 1130

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*
- 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1130	100.0	1130	13	ADR73675	Adr73675 Rice prom
2	1130	100.0	1606	14	AEC16154	Aec16154 Rice HMGI
3	231	20.4	998	14	AEC16155	Aec16155 Rice HMGI
4	158.6	14.0	812	10	ADK58252	Adk58252 Plant DNA
5	119.8	10.6	964	13	ADR73697	Adr73697 Rice prom
6	115	10.2	871	2	AAV12741	Aav12741 RBE1 tran
7	96.6	8.5	797	10	ADK58241	Adk58241 Plant DNA
8	80	7.1	595	10	ADK54154	Adk54154 Plant DNA
9	79	7.0	622	10	ADK54152	Adk54152 Plant DNA
10	58.8	5.2	13700	4	AAD18808	Aad18808 Human gen
11	58.8	5.2	37278	13	ABD33082	Abd33082 Murine ca
12	58.8	5.2	73308	6	ABL66966	Abl66966 Lung canc
13	58.2	5.2	75782	12	ADQ97795	Adq97795 Mouse can
c 14	58	5.1	5935	3	AAA28818	Aaa28818 Murine T
c 15	58	5.1	5935	4	AAS14878	Aas14878 Mouse par
c 16	58	5.1	5935	6	AAD30660	Aad30660 Mouse TIF
c 17	58	5.1	5935	6	AAD27153	Aad27153 Mouse T c
c 18	58	5.1	5935	12	ADP84671	Adp84671 Mouse TIF
c 19	57.8	5.1	203132	13	ABD33364	Abd33364 Murine ca
c 20	57.8	5.1	203132	14	ADZ13443	Adz13443 Murine ca
21	55.4	4.9	37185	13	ADW39406	Adw39406 Herpes si
22	55.4	4.9	152261	14	AEC07415	Aec07415 DNA of HS
23	55.4	4.9	152261	14	AED00550	Aed00550 Herpes so
c 24	54.8	4.8	242496	14	AED76150	Aed76150 Mouse CA
c 25	54.4	4.8	326002	13	ABD32843	Abd32843 Human can
c 26	53.8	4.8	40772	13	ADW39403	Adw39403 Herpes si
c 27	53.8	4.8	152261	14	AEC07415	Aec07415 DNA of HS
c 28	53.8	4.8	152261	14	AED00550	Aed00550 Herpes so
29	53.6	4.7	64482	12	ADQ59515	Adq59515 Human can
30	53.6	4.7	64482	14	ADZ13896	Adz13896 Murine ca
31	53.4	4.7	110000	13	ABD32594_4	Continuation (5 of
c 32	53.2	4.7	100100	15	AEF07226	Aef07226 LOC115209
33	52.6	4.7	2280	15	AEE83824	Aee83824 Human cDN
c 34	52.6	4.7	260209	6	ABS56564	Abs56564 Human SUL
c 35	52.6	4.7	260209	12	ADN16204	Adn16204 Human sul
36	52.4	4.6	3163	10	ADC87060	Adc87060 Human GPC
37	52	4.6	53522	6	AAD30228	Aad30228 Human PKD
38	52	4.6	53522	13	ADU03973	Adu03973 Human pol
39	52	4.6	53522	14	AEB35216	Aeb35216 Human Gef
40	52	4.6	53526	2	AAT94101	Aat94101 Human PKD
41	52	4.6	53577	2	AAT18551	Aat18551 Human pol
42	52	4.6	53577	2	AAT94108	Aat94108 Human PKD
43	52	4.6	106315	11	ACN43966	Acn43966 Human gen
c 44	51.8	4.6	5452	10	ADC86736	Adc86736 Human GPC
45	51.6	4.6	110000	13	ABD32921_2	Continuation (3 of

## ALIGNMENTS

RESULT 1  
ADR73675

# SCORE Search Results Details for Application 10525647 and Search Result us-10-525-647- 18.rng.

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OM nucleic - nucleic search, using sw model

Run on: August 31, 2006, 00:10:55 ; Search time 842 Seconds  
(without alignments)  
9357.056 Million cell updates/sec

Title: US-10-525-647-18

Perfect score: 1130

Sequence: 1 catgcggctaatgttagatgc.....ccttctcgccaggattcagcc 1130

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8:\*

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
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7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1130	100.0	1130	13	ADR73675	Adr73675 Rice prom
2	1130	100.0	1606	14	AEC16154	Aec16154 Rice HMG1
3	231	20.4	998	14	AEC16155	Aec16155 Rice HMG1
4	158.6	14.0	812	10	ADK58252	Adk58252 Plant DNA
5	119.8	10.6	964	13	ADR73697	Adr73697 Rice prom
6	115	10.2	871	2	AAV12741	Aav12741 RBE1 tran
7	96.6	8.5	797	10	ADK58241	Adk58241 Plant DNA
8	80	7.1	595	10	ADK54154	Adk54154 Plant DNA
9	79	7.0	622	10	ADK54152	Adk54152 Plant DNA
10	58.8	5.2	13700	4	AAD18808	Aad18808 Human gen
11	58.8	5.2	37278	13	ABD33082	Abd33082 Murine ca
12	58.8	5.2	73308	6	ABL66966	Abl66966 Lung canc
13	58.2	5.2	75782	12	ADQ97795	Adq97795 Mouse can
c 14	58	5.1	5935	3	AAA28818	Aaa28818 Murine T
c 15	58	5.1	5935	4	AAS14878	Aas14878 Mouse par
c 16	58	5.1	5935	6	AAD30660	Aad30660 Mouse TIF
c 17	58	5.1	5935	6	AAD27153	Aad27153 Mouse T c
c 18	58	5.1	5935	12	ADP84671	Adp84671 Mouse TIF
c 19	57.8	5.1	203132	13	ABD33364	Abd33364 Murine ca
c 20	57.8	5.1	203132	14	ADZ13443	Adz13443 Murine ca
21	55.4	4.9	37185	13	ADW39406	Adw39406 Herpes si
22	55.4	4.9	152261	14	AEC07415	Aec07415 DNA of HS
23	55.4	4.9	152261	14	AED00550	Aed00550 Herpes so
c 24	54.8	4.8	242496	14	AED76150	Aed76150 Mouse CA
c 25	54.4	4.8	326002	13	ABD32843	Abd32843 Human can
c 26	53.8	4.8	40772	13	ADW39403	Adw39403 Herpes si
c 27	53.8	4.8	152261	14	AEC07415	Aec07415 DNA of HS
c 28	53.8	4.8	152261	14	AED00550	Aed00550 Herpes so
29	53.6	4.7	64482	12	ADQ59515	Adq59515 Human can
30	53.6	4.7	64482	14	ADZ13896	Adz13896 Murine ca
31	53.4	4.7	110000	13	ABD32594_4	Continuation (5 of
c 32	53.2	4.7	100100	15	AEF07226	Aef07226 LOC115209
33	52.6	4.7	2280	15	AEE83824	Aee83824 Human cDN
c 34	52.6	4.7	260209	6	ABS56564	Abs56564 Human SUL
c 35	52.6	4.7	260209	12	ADN16204	Adn16204 Human sul
36	52.4	4.6	3163	10	ADC87060	Adc87060 Human GPC
37	52	4.6	53522	6	AAD30228	Aad30228 Human PKD
38	52	4.6	53522	13	ADU03973	Adu03973 Human pol
39	52	4.6	53522	14	AEB35216	Aeb35216 Human Gef
40	52	4.6	53526	2	AAT94101	Aat94101 Human PKD
41	52	4.6	53577	2	AAT18551	Aat18551 Human pol
42	52	4.6	53577	2	AAT94108	Aat94108 Human PKD
43	52	4.6	106315	11	ACN43966	Acn43966 Human gen
c 44	51.8	4.6	5452	10	ADC86736	Adc86736 Human GPC
45	51.6	4.6	110000	13	ABD32921_2	Continuation (3 of

## ALIGNMENTS

RESULT 1  
ADR73675

# SCORE Search Results Details for Application 10525647 and Search Result us-10-525-647-18.

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OM nucleic - nucleic search, using sw model

Run on: August 31, 2006, 00:28:40 ; Search time 278 Seconds  
(without alignments)  
7605.586 Million cell updates/sec

Title: US-10-525-647-18  
Perfect score: 1130  
Sequence: 1 catgcggctaatgttagatgc.....ccttctcgaggattcagcc 1130

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*  
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8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result	Query				
No.	Score	Match Length	DB	ID	Description

1	82.6	7.3	7218	2	US-08-232-463-14	Sequence 14, Appl
c 2	74	6.5	7218	2	US-08-232-463-14	Sequence 14, Appl
3	58.8	5.2	5650	3	US-09-949-016-14008	Sequence 14008, A
c 4	58	5.1	5935	3	US-09-178-973B-17	Sequence 17, Appl
c 5	58	5.1	5935	3	US-09-419-568F-29	Sequence 29, Appl
c 6	58	5.1	5935	3	US-09-354-243B-29	Sequence 29, Appl
7	57.2	5.1	936	3	US-09-270-767-4464	Sequence 4464, Ap
8	57.2	5.1	936	3	US-09-270-767-19746	Sequence 19746, A
9	56.2	5.0	264665	3	US-09-949-016-13747	Sequence 13747, A
c 10	54.4	4.8	1583	3	US-09-270-767-11302	Sequence 11302, A
c 11	53.4	4.7	12703	3	US-09-949-016-16685	Sequence 16685, A
c 12	52.2	4.6	767677	3	US-09-949-016-12147	Sequence 12147, A
c 13	52.2	4.6	767677	3	US-09-949-016-17361	Sequence 17361, A
14	52	4.6	53526	3	US-08-658-136-2	Sequence 2, Appli
15	52	4.6	53577	3	US-08-658-136-1	Sequence 1, Appli
16	52	4.6	53577	3	US-08-460-215A-1	Sequence 1, Appli
17	51.4	4.5	422592	3	US-09-949-016-14182	Sequence 14182, A
18	50.8	4.5	2674	3	US-09-019-095A-1	Sequence 1, Appli
19	50.8	4.5	23802	3	US-09-949-016-12107	Sequence 12107, A
20	50.8	4.5	23803	3	US-09-949-016-15878	Sequence 15878, A
c 21	50.8	4.5	47471	3	US-09-949-016-12271	Sequence 12271, A
c 22	50.8	4.5	113283	3	US-09-949-016-16976	Sequence 16976, A
c 23	50.8	4.5	113283	3	US-09-949-016-16977	Sequence 16977, A
c 24	50.8	4.5	119649	3	US-09-949-016-12537	Sequence 12537, A
c 25	50.6	4.5	270	3	US-09-443-282B-32	Sequence 32, Appl
c 26	49.2	4.4	254	3	US-09-443-282B-33	Sequence 33, Appl
c 27	49	4.3	289	3	US-09-007-005-17	Sequence 17, Appl
c 28	49	4.3	289	3	US-09-244-796-17	Sequence 17, Appl
29	48.8	4.3	38920	3	US-09-949-016-17546	Sequence 17546, A
c 30	48.8	4.3	106199	3	US-09-949-016-12393	Sequence 12393, A
c 31	48.2	4.3	390416	3	US-09-949-016-16923	Sequence 16923, A
32	48.2	4.3	462589	3	US-09-949-016-12900	Sequence 12900, A
33	48.2	4.3	476044	3	US-09-949-016-12412	Sequence 12412, A
34	48	4.2	390890	3	US-09-949-016-14720	Sequence 14720, A
35	47.8	4.2	51252	3	US-09-949-016-16348	Sequence 16348, A
36	47.6	4.2	53336	3	US-09-949-016-12500	Sequence 12500, A
37	47.6	4.2	53337	3	US-09-949-016-16092	Sequence 16092, A
c 38	47.2	4.2	601	3	US-09-949-016-80587	Sequence 80587, A
c 39	47.2	4.2	601	3	US-09-949-016-80588	Sequence 80588, A
c 40	47.2	4.2	421491	3	US-09-949-016-12805	Sequence 12805, A
c 41	47.2	4.2	421494	3	US-09-949-016-14060	Sequence 14060, A
c 42	47	4.2	1377	2	US-08-810-572A-1	Sequence 1, Appli
c 43	47	4.2	1377	3	US-09-290-333-1	Sequence 1, Appli
c 44	47	4.2	1377	3	US-09-782-857A-1	Sequence 1, Appli
c 45	47	4.2	1377	3	US-09-879-919-21	Sequence 21, Appli

## ALIGNMENTS

## RESULT 1

US-08-232-463-14  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52

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18.rnpbm.

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OM nucleic - nucleic search, using sw model

Run on: August 31, 2006, 00:29:14 ; Search time 2071 Seconds  
(without alignments)  
6704.504 Million cell updates/sec

Title: US-10-525-647-18  
Perfect score: 1130  
Sequence: 1 catgcggctaatgttagatgc.....ccttctcgcaggattcagcc 1130

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA\_Main:\*

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8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	158.6	14.0	812	10	US-10-487-901-5635	Sequence 5635, Ap
2	96.6	8.5	797	10	US-10-487-901-5624	Sequence 5624, Ap
3	96.4	8.5	345	8	US-10-437-963-29124	Sequence 29124, A
4	94	8.3	272	8	US-10-437-963-241	Sequence 241, App
5	80	7.1	595	10	US-10-487-901-1537	Sequence 1537, Ap
6	79	7.0	622	10	US-10-487-901-1535	Sequence 1535, Ap
7	67.8	6.0	680	8	US-10-437-963-100767	Sequence 100767,
8	65	5.8	601	8	US-10-437-963-40982	Sequence 40982, A
9	58.8	5.2	13700	6	US-10-220-310-2	Sequence 2, Appli
10	58.8	5.2	37278	8	US-10-322-281-21	Sequence 21, Appl
11	58.8	5.2	73308	3	US-09-954-456-2276	Sequence 2276, Ap
12	58.8	5.2	73308	10	US-10-843-641A-5303	Sequence 5303, Ap
13	58.2	5.2	75782	11	US-10-330-773-772	Sequence 772, App
c 14	58	5.1	5935	3	US-09-751-797-29	Sequence 29, Appl
c 15	58	5.1	5935	8	US-10-627-273-29	Sequence 29, Appl
c 16	58	5.1	5935	15	US-11-177-987-42	Sequence 42, Appl
c 17	57.8	5.1	203132	8	US-10-322-281-459	Sequence 459, App
18	56.6	5.0	769	8	US-10-437-963-79660	Sequence 79660, A
c 19	56.2	5.0	448	9	US-10-674-124A-23814	Sequence 23814, A
c 20	56.2	5.0	126552	15	US-11-121-086-1	Sequence 1, Appli
c 21	54.4	4.8	462	9	US-10-674-124A-19244	Sequence 19244, A
22	54.4	4.8	595	6	US-10-027-632-186134	Sequence 186134,
23	54.4	4.8	595	6	US-10-027-632-293620	Sequence 293620,
24	54.4	4.8	595	6	US-10-027-632-293621	Sequence 293621,
25	54.4	4.8	595	6	US-10-027-632-293622	Sequence 293622,
26	54.4	4.8	595	7	US-10-027-632-186134	Sequence 186134,
27	54.4	4.8	595	7	US-10-027-632-293620	Sequence 293620,
28	54.4	4.8	595	7	US-10-027-632-293621	Sequence 293621,
29	54.4	4.8	595	7	US-10-027-632-293622	Sequence 293622,
c 30	54.4	4.8	326002	10	US-10-461-862-56	Sequence 56, Appl
31	54.2	4.8	420	12	US-10-301-480-565366	Sequence 565366,
32	54.2	4.8	420	12	US-10-301-480-1178775	Sequence 1178775,
33	54.2	4.8	599	10	US-10-972-079-64751	Sequence 64751, A
34	53.6	4.7	64482	8	US-10-322-696-151	Sequence 151, App
35	53.4	4.7	684187	8	US-10-367-094-71	Sequence 71, Appl
36	53.2	4.7	595	6	US-10-027-632-71055	Sequence 71055, A
37	53.2	4.7	595	6	US-10-027-632-71056	Sequence 71056, A
38	53.2	4.7	595	6	US-10-027-632-71057	Sequence 71057, A
39	53.2	4.7	595	7	US-10-027-632-71055	Sequence 71055, A
40	53.2	4.7	595	7	US-10-027-632-71056	Sequence 71056, A
41	53.2	4.7	595	7	US-10-027-632-71057	Sequence 71057, A
42	53.2	4.7	808	6	US-10-027-632-38795	Sequence 38795, A
43	53.2	4.7	808	6	US-10-027-632-38796	Sequence 38796, A
44	53.2	4.7	808	6	US-10-027-632-38797	Sequence 38797, A
45	53.2	4.7	808	7	US-10-027-632-38795	Sequence 38795, A

## ALIGNMENTS

RESULT 1  
US-10-487-901-5635

# SCORE Search Results Details for Application 10525647 and Search Result us-10-525-647. 18.rnpbn.

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This page gives you Search Results detail for the Application 10525647 and Search Result us-10-5:18.rnpbn.

[start](#)

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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 31, 2006, 00:39:45 ; Search time 491 Seconds  
(without alignments)  
3795.052 Million cell updates/sec

Title: US-10-525-647-18  
Perfect score: 1130  
Sequence: 1 catgcggctaatgttagatgc.....ccttctcgcaggattcagcc 1130

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2281053 seqs, 824500224 residues

Total number of hits satisfying chosen parameters: 4562106

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA\_New:  
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3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq1:\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Query					Description
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1	1130	100.0	1130	6	US-10-525-647-18	Sequence 18, Appl
2	231	20.4	998	6	US-10-449-902-18506	Sequence 18506, A
3	139	12.3	913	6	US-10-449-902-5027	Sequence 5027, Ap
4	119.8	10.6	964	6	US-10-525-647-40	Sequence 40, Appl
5	58.8	5.2	37278	6	US-10-539-228-21	Sequence 21, Appl
6	58.2	5.2	75782	6	US-10-540-898-772	Sequence 772, App
c 7	57.8	5.1	203132	6	US-10-539-228-459	Sequence 459, App
8	51.4	4.5	1421559	8	US-11-266-748A-28208	Sequence 28208, A
9	51.2	4.5	3892	8	US-11-266-748A-24151	Sequence 24151, A
10	51.2	4.5	55906	6	US-10-539-228-417	Sequence 417, App
c 11	51.2	4.5	96861	6	US-10-540-898-811	Sequence 811, App
12	50.8	4.5	47286	6	US-10-540-898-651	Sequence 651, App
c 13	50	4.4	4647455	6	US-10-641-321-205	Sequence 205, App
c 14	49.4	4.4	340000	8	US-11-266-748A-61353	Sequence 61353, A
15	49.4	4.4	634888	6	US-10-533-365-1	Sequence 1, Appli
16	49.2	4.4	194186	6	US-10-540-898-395	Sequence 395, App
c 17	49	4.3	199868	6	US-10-540-898-808	Sequence 808, App
18	48.2	4.3	195102	6	US-10-733-042-1	Sequence 1, Appli
c 19	48	4.2	2834	8	US-11-266-748A-23491	Sequence 23491, A
c 20	47.8	4.2	37790	6	US-10-519-505-1	Sequence 1, Appli
c 21	47.8	4.2	38166	6	US-10-519-505-2	Sequence 2, Appli
22	47.8	4.2	92219	6	US-10-539-228-805	Sequence 805, App
23	47.8	4.2	205388	6	US-10-540-898-537	Sequence 537, App
c 24	47.6	4.2	623	6	US-10-533-365-47	Sequence 47, Appl
c 25	47.6	4.2	25229	6	US-10-540-898-202	Sequence 202, App
26	47.2	4.2	45736	6	US-10-539-228-767	Sequence 767, App
c 27	47	4.2	1377	8	US-11-318-156-1	Sequence 1, Appli
c 28	47	4.2	1377	8	US-11-266-748A-22727	Sequence 22727, A
29	46.8	4.1	958	8	US-11-266-748A-59001	Sequence 59001, A
30	46.8	4.1	95484	6	US-10-540-898-275	Sequence 275, App
c 31	46.6	4.1	84410	6	US-10-539-228-747	Sequence 747, App
32	46.6	4.1	96861	6	US-10-540-898-811	Sequence 811, App
33	46.4	4.1	5627	8	US-11-266-748A-28459	Sequence 28459, A
c 34	46.4	4.1	45764	6	US-10-540-898-251	Sequence 251, App
35	46.4	4.1	97081	6	US-10-540-898-957	Sequence 957, App
c 36	46.4	4.1	105357	8	US-11-266-748A-61429	Sequence 61429, A
37	46.2	4.1	1000	8	US-11-266-748A-283673	Sequence 283673,
c 38	46.2	4.1	1000	8	US-11-266-748A-335102	Sequence 335102,
39	46.2	4.1	1000	8	US-11-266-748A-393443	Sequence 393443,
c 40	46.2	4.1	1000	8	US-11-266-748A-464489	Sequence 464489,
c 41	46.2	4.1	32495	6	US-10-539-228-401	Sequence 401, App
42	46.2	4.1	58320	6	US-10-539-228-88	Sequence 88, Appl
c 43	46	4.1	28449	6	US-10-540-898-216	Sequence 216, App
44	46	4.1	687411	6	US-10-540-898-26	Sequence 26, Appl
45	45.6	4.0	1000	8	US-11-266-748A-199492	Sequence 199492,

## ALIGNMENTS

## RESULT 1

US-10-525-647-18  
; Sequence 18, Application US/10525647  
; Publication No. US20060112442A1  
; GENERAL INFORMATION:  
; APPLICANT: CropDesign N.V.  
; TITLE OF INVENTION: Rice promoters  
; FILE REFERENCE: CD-071-PCT

# SCORE Search Results Details for Application 10525647 and Search Result us-10-525-647- 18.rst.

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OM nucleic - nucleic search, using sw model

Run on: August 31, 2006, 00:23:09 ; Search time 6175 Seconds  
(without alignments)  
10233.011 Million cell updates/sec

Title: US-10-525-647-18

Perfect score: 1130

Sequence: 1 catgcggctaatgttagatgc.....ccttctcgccaggattcagcc 1130

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:  
2: gb\_est3:  
3: gb\_est4:  
4: gb\_est5:  
5: gb\_est6:  
6: gb\_htc:  
7: gb\_est2:  
8: gb\_est7:  
9: gb\_est8:  
10: gb\_est9:  
11: gb\_gss1:  
12: gb\_gss2:  
13: gb\_gss3:  
14: gb\_gss4:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	168.4	14.9	440	5	CF292390	CF292390 30DGS--01
2	166.2	14.7	608	5	CK059774	CK059774 52424sice
3	165	14.6	574	5	CF279360	CF279360 14ETL--05
4	165	14.6	615	5	CF314657	CF314657 HD--03-E0
5	158	14.0	859	4	CB675811	CB675811 OSJNEe11M
6	156.4	13.8	297	5	CK006362	CK006362 26976rsic
7	153.4	13.6	591	5	CF963422	CF963422 10813rsic
8	151.4	13.4	655	4	CB685301	CB685301 OSJNEf15J
9	147	13.0	618	5	CK078094	CK078094 82374rsic
10	145.8	12.9	533	5	CF281141	CF281141 14ETL--08
11	145	12.8	603	5	CF282431	CF282431 14ETL--09
12	144	12.7	432	5	CF277714	CF277714 14ETL--03
13	144	12.7	569	5	CF282280	CF282280 14ETL--09
14	144	12.7	651	5	CF291071	CF291071 14ROOT--0
15	144	12.7	660	5	CF292534	CF292534 30DGS--01
16	140	12.4	575	5	CF312650	CF312650 ABF--08-H
17	140	12.4	576	5	CF296977	CF296977 30DGS--07
18	140	12.4	586	5	CF295516	CF295516 30DGS--05
19	140	12.4	608	5	CF308019	CF308019 ABF--01-K
20	140	12.4	612	5	CF312423	CF312423 ABF--08-C
21	140	12.4	646	5	CF312873	CF312873 ABF--08-M
22	140	12.4	647	5	CF277047	CF277047 14ETL--02
23	139	12.3	492	5	CF277720	CF277720 14ETL--03
24	139	12.3	555	5	CF312341	CF312341 ABF--07-P
25	139	12.3	575	5	CF311877	CF311877 ABF--07-F
26	139	12.3	576	5	CF291117	CF291117 14ROOT--0
27	139	12.3	591	5	CF281129	CF281129 14ETL--08
28	139	12.3	622	5	CF277475	CF277475 14ETL--03
29	139	12.3	652	5	CF293518	CF293518 30DGS--02
30	138.4	12.2	366	5	CF292295	CF292295 30DGS--01
c 31	138.2	12.2	824	13	CW632541	CW632541 OP_Ba006
32	137.4	12.2	551	5	CF308482	CF308482 ABF--02-F
33	137	12.1	572	5	CF282296	CF282296 14ETL--09
34	137	12.1	621	5	CF279594	CF279594 14ETL--05
35	137	12.1	657	5	CF292592	CF292592 30DGS--01
36	137	12.1	670	5	CF277460	CF277460 14ETL--03
37	136	12.0	295	5	CI298665	CI298665 CI298665
38	136	12.0	309	5	CF296107	CF296107 30DGS--06
39	136	12.0	311	8	CV732879	CV732879 FLO--07-I
40	136	12.0	348	5	CI300124	CI300124 CI300124
41	136	12.0	355	8	CV729959	CV729959 FLO--03-E
42	136	12.0	358	5	CF308797	CF308797 ABF--02-M
43	136	12.0	394	5	CI288540	CI288540 CI288540
44	136	12.0	402	5	CF295060	CF295060 30DGS--04
45	136	12.0	423	5	CF296753	CF296753 30DGS--07

## ALIGNMENTS

## RESULT 1

CF292390

LOCUS

CF292390

440 bp

mRNA

linear

EST 14-AUG-2003